

# SEQUENCE LISTING

<110> SEIKI, Motoharu  
SATO, Hiroshi  
SHINAGAWA, Akira

<120> NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR

<130> 55-290P

<140> 08/448,489

<141> 1995-06-07

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 582

<212> PRT

<213> Homo sapiens

<400> 1

Met Ser Pro Ala Pro Arg Pro Ser Arg Cys Leu Leu Leu Pro Leu Leu  
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Thr Leu Gly Thr Ala Leu Ala Ser Leu Gly Ser Ala Gln Ser Ser Ser  
20 25 30

Phe Ser Pro Glu Ala Trp Leu Gln Gln Tyr Gly Tyr Leu Pro Pro Gly  
35 40 45

Asp Leu Arg Thr His Thr Gln Arg Ser Pro Gln Ser Leu Ser Ala Ala  
50 55 60

Ile Ala Ala Met Gln Lys Phe Tyr Gly Leu Gln Val Thr Gly Lys Ala  
65 70 75 80

Asp Ala Asp Thr Met Lys Ala Met Arg Arg Pro Arg Cys Gly Val Pro  
85 90 95

Asp Lys Phe Gly Ala Glu Ile Lys Ala Asn Val Arg Arg Lys Arg Tyr  
100 105 110

Ala Ile Gln Gly Leu Lys Trp Gln His Asn Glu Ile Thr Phe Cys Ile  
115 120 125

Gln Asn Tyr Thr Pro Lys Val Gly Glu Tyr Ala Thr Tyr Glu Ala Ile

130	135	140
Arg Lys Ala Phe Arg Val Trp Glu Ser Ala Thr Pro Leu Arg Phe Arg		
145	150	155 160
Glu Val Pro Tyr Ala Tyr Ile Arg Glu Gly His Glu Lys Gln Ala Asp		
165	170	175
Ile Met Ile Phe Phe Ala Glu Gly Phe His Gly Asp Ser Thr Pro Phe		
180	185	190
Asp Gly Glu Gly Gly Phe Leu Ala His Ala Tyr Phe Pro Gly Pro Asn		
195	200	205
Ile Gly Gly Asp Thr His Phe Asp Ser Ala Glu Pro Trp Thr Val Arg		
210	215	220
Asn Glu Asp Leu Asn Gly Asn Asp Ile Phe Leu Val Ala Val His Glu		
225	230	235 240
Leu Gly His Ala Leu Gly Leu Glu His Ser Ser Asp Pro Ser Ala Ile		
245	250	255
Met Ala Pro Phe Tyr Gln Trp Met Asp Thr Glu Asn Phe Val Leu Pro		
260	265	270
Asp Asp Asp Arg Arg Gly Ile Gln Gln Leu Tyr Gly Gly Glu Ser Gly		
275	280	285
Phe Pro Thr Lys Met Pro Pro Gln Pro Arg Thr Thr Ser Arg Pro Ser		
290	295	300
Val Pro Asp Lys Pro Lys Asn Pro Thr Tyr Gly Pro Asn Ile Cys Asp		
305	310	315 320
Gly Asn Phe Asp Thr Val Ala Met Leu Arg Gly Glu Met Phe Val Phe		
325	330	335
Lys Lys Arg Trp Phe Trp Arg Val Arg Asn Asn Gln Val Met Asp Gly		
340	345	350
Tyr Pro Met Pro Ile Gly Gln Phe Trp Arg Gly Leu Pro Ala Ser Ile		
355	360	365
Asn Thr Ala Tyr Glu Arg Lys Asp Gly Lys Phe Val Phe Phe Lys Gly		
370	375	380
Asp Lys His Trp Val Phe Asp Glu Ala Ser Leu Glu Pro Gly Tyr Pro		

385                      390                      395                      400  
 Lys His Ile Lys Glu Leu Gly Arg Gly Leu Pro Thr Asp Lys Ile Asp  
                          405                      410                      415  
 Ala Ala Leu Phe Trp Met Pro Asn Gly Lys Thr Tyr Phe Phe Arg Gly  
                          420                      425                      430  
 Asn Lys Tyr Tyr Arg Phe Asn Glu Glu Leu Arg Ala Val Asp Ser Glu  
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 Tyr Pro Lys Asn Ile Lys Val Trp Glu Gly Ile Pro Glu Ser Pro Arg  
                          450                      455                      460  
 Gly Ser Phe Met Gly Ser Asp Glu Val Phe Thr Tyr Phe Tyr Lys Gly  
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 Asn Lys Tyr Trp Lys Phe Asn Asn Gln Lys Leu Lys Val Glu Pro Gly  
                          485                      490                      495  
 Tyr Pro Lys Ser Ala Leu Arg Asp Trp Met Gly Cys Pro Ser Gly Gly  
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 Arg Pro Asp Glu Gly Thr Glu Glu Glu Thr Glu Val Ile Ile Ile Glu  
                          515                      520                      525  
 Val Asp Glu Glu Gly Gly Gly Ala Val Ser Ala Ala Ala Val Val Leu  
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 Pro Val Leu Leu Leu Leu Leu Val Leu Ala Val Gly Leu Ala Val Phe  
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 Phe Phe Arg Arg His Gly Thr Pro Arg Arg Leu Leu Tyr Cys Gln Arg  
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 Ser Leu Leu Asp Lys Val  
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<210> 2

<211> 3403

<212> DNA

<213> Homo sapiens

<400> 2

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 gcccgaagac cctccggtg tctctgctc ccctgctca cgctcgac cgcgctcgcc 180

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tacctgctc	ccggggacct	acgtaccac	acacagcgct	caccccagtc	actctcagcg	300
gccatcgctg	ccatgcagaa	gttttacggc	ttgcaagtaa	caggcaaagc	tgatgcagac	360
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gcagtggata	gcgagtaccc	caagaacatc	aaagtctggg	aagggatccc	tgagtctccc	1500
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cctctcgaat	gttagccttg	gatggggctt	tcacagttag	aagagctgaa	accaggggtg	2640
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cacaaacgag	gaatgagggg	cttcacgaga	ggccacaggg	cctggctggc	cacgctgtcc	3060

cggcctgctc accatctcag tgagggacag gagctggggc tgcttaggct ggggtccacgc 3120  
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 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: Highly conserved  
 sequence fragments from MMP family

<400> 3  
 Pro Arg Cys Gly Val Pro Asp  
 1 5

<210> 4  
 <211> 9  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: Highly conserved  
 sequence fragments from MMP family

<400> 4  
 Gly Asp Ala His Phe Asp Asp Asp Glu  
 1 5

<210> 5  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic DNA

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 cmmgvtgys gvrwbccwga

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<210> 6  
 <211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 6

ytcrtsvtcr tcraartgrr hrtcy

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<210> 7

<211> 30

<212> PRT

<213> Homo sapiens

<400> 7

Gly Gly Ala Val Ser Ala Ala Ala Val Val Leu Pro Val Leu Leu  
1 5 10 15

Leu Leu Leu Val Leu Ala Val Gly Leu Ala Val Phe Phe Phe  
20 25 30

<210> 8

<211> 14

<212> PRT

<213> Homo sapiens

<400> 8

Arg Glu Val Pro Tyr Ala Tyr Ile Arg Glu Gly His Glu Lys  
1 5 10

<210> 9

<211> 14

<212> PRT

<213> Homo sapiens

<400> 9

Asp Gly Asn Phe Asp Thr Val Ala Met Leu Arg Gly Glu Met  
1 5 10

<210> 10

<211> 15

<212> PRT

<213> Homo sapiens

<400> 10

Pro Lys Ser Ala Leu Arg Asp Trp Met Gly Cys Pro Ser Gly Gly  
 1 5 10 15

<210> 11  
 <211> 489  
 <212> PRT  
 <213> Unknown

<220>  
 <223> X = UNKNOWN

<220>  
 <223> Description of Unknown Organism: Known Member of  
 Matrix Metalloproteinase Family

<400> 11  
 Met Ala Pro Ala Ala Trp Leu Arg Ser Ala Ala Ala Arg Ala Leu Leu  
 1 5 10 15

Pro Pro Met Leu Leu Leu Leu Gln Pro Pro Pro Leu Leu Ala Arg  
 20 25 30

Ala Leu Pro Pro Asp Val His His Leu His Ala Glu Arg Arg Gly Pro  
 35 40 45

Gln Pro Trp His Ala Ala Leu Pro Ser Ser Pro Ala Pro Ala Pro Ala  
 50 55 60

Thr Gln Glu Ala Pro Arg Pro Ala Ser Ser Leu Arg Pro Pro Arg Cys  
 65 70 75 80

Gly Val Pro Asp Pro Ser Asp Gly Leu Ser Ala Arg Asn Arg Gln Lys  
 85 90 95

Arg Phe Val Leu Ser Gly Gly Arg Trp Glu Lys Thr Asp Leu Thr Tyr  
 100 105 110

Arg Ile Leu Arg Phe Pro Trp Gln Leu Val Gln Glu Gln Val Arg Gln  
 115 120 125

Thr Met Ala Glu Ala Leu Lys Val Trp Ser Asp Val Thr Pro Leu Thr  
 130 135 140

Phe Thr Glu Val His Glu Gly Arg Ala Asp Ile Met Ile Asp Phe Ala  
 145 150 155 160

Arg Tyr Trp Asp Gly Asp Asp Leu Pro Phe Asp Gly Pro Gly Gly Ile

165

170

175

Leu Ala His Ala Phe Phe Pro Lys Thr His Arg Glu Gly Asp Val His  
180 185 190

Phe Asp Tyr Asp Glu Thr Trp Thr Ile Gly Asp Asp Gln Gly Thr Asp  
195 200 205

Leu Leu Gln Val Ala Ala His Glu Phe Gly His Val Leu Gly Leu Gln  
210 215 220

His Thr Thr Ala Ala Lys Ala Leu Met Ser Ala Phe Tyr Thr Phe Arg  
225 230 235 240

Tyr Pro Leu Ser Leu Ser Pro Asp Asp Cys Arg Gly Val Gln His Leu  
245 250 255

Tyr Gly Gln Pro Trp Pro Thr Val Thr Ser Arg Thr Pro Ala Leu Gly  
260 265 270

Pro Gln Ala Gly Ile Asp Thr Asn Glu Ile Ala Pro Leu Glu Pro Asp  
275 280 285

Ala Pro Pro Asp Ala Cys Glu Ala Ser Phe Asp Ala Val Ser Thr Ile  
290 295 300

Arg Gly Glu Leu Phe Phe Phe Lys Ala Gly Phe Val Trp Arg Leu Arg  
305 310 315 320

Gly Gly Gln Leu Gln Pro Gly Tyr Pro Ala Leu Ala Ser Arg His Trp  
325 330 335

Gln Gly Leu Pro Ser Pro Val Asp Ala Ala Phe Glu Asp Ala Gln Gly  
340 345 350

His Ile Trp Phe Phe Gln Gly Ala Gln Tyr Trp Val Tyr Asp Gly Glu  
355 360 365

Lys Pro Val Leu Gly Pro Ala Pro Leu Thr Glu Leu Gly Leu Val Arg  
370 375 380

Phe Pro Val His Ala Ala Leu Val Trp Gly Pro Glu Lys Asn Lys Ile  
385 390 395 400

Tyr Phe Phe Arg Gly Arg Asp Tyr Trp Arg Phe His Pro Ser Thr Arg  
405 410 415

Arg Val Asp Ser Pro Val Pro Arg Arg Ala Thr Asp Trp Arg Gly Val



420

425

430

Pro Ser Glu Ile Asp Ala Ala Phe Gln Asp Ala Asp Gly Tyr Ala Tyr  
 435 440 445

Phe Leu Arg Gly Arg Leu Tyr Trp Lys Phe Asp Pro Val Lys Val Lys  
 450 455 460

Ala Leu Glu Gly Phe Pro Arg Leu Val Gly Pro Asp Phe Phe Gly Cys  
 465 470 475 480

Ala Glu Pro Ala Asn Thr Phe Leu Xaa  
 485

&lt;210&gt; 12

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

<223> Description of Unknown Organism: Known Member of  
 Matrix Metalloproteinase Family

&lt;400&gt; 12

Met His Ser Phe Pro Pro Leu Leu Leu Leu Leu Phe Trp Gly Val Val  
 1 5 10 15

Ser His Ser Phe Pro Ala Thr Leu Glu Thr Gln Glu Gln Asp Val Asp  
 20 25 30

Leu Val Gln Lys Tyr Leu Glu Lys Tyr Tyr Asn Leu Lys Asn Asp Gly  
 35 40 45

Arg Gln Val Glu Lys Arg Arg Asn Ser Gly Pro Val Val Glu Lys Leu  
 50 55 60

Lys Gln Met Gln Glu Phe Phe Gly Leu Lys Val Thr Gly Lys Pro Asp  
 65 70 75 80

Ala Glu Thr Leu Lys Val Met Lys Gln Pro Arg Cys Gly Val Pro Asp  
 85 90 95

Val Ala Gln Phe Val Leu Thr Glu Gly Asn Pro Arg Trp Glu Gln Thr  
 100 105 110

His Leu Thr Tyr Arg Ile Glu Asn Tyr Thr Pro Asp Leu Pro Arg Ala  
 115 120 125

Asp Val Asp His Ala Ile Glu Lys Ala Phe Gln Leu Trp Ser Asn Val  
 130 135 140

Thr Pro Leu Thr Phe Thr Lys Val Ser Glu Gly Gln Ala Asp Ile Met  
 145 150 155 160

Ile Ser Phe Val Arg Gly Asp His Arg Asp Asn Ser Pro Phe Asp Gly  
 165 170 175

Pro Gly Gly Asn Leu Ala His Ala Phe Gln Pro Gly Pro Gly Ile Gly  
 180 185 190

Gly Asp Ala His Phe Asp Glu Asp Glu Arg Trp Thr Asn Asn Phe Thr  
 195 200 205

Glu Tyr Asn Leu His Arg Val Ala Ala His Glu Leu Gly His Ser Leu  
 210 215 220

Gly Leu Ser His Ser Thr Asp Ile Gly Ala Leu Met Tyr Pro Ser Tyr  
 225 230 235 240

Thr Phe Ser Gly Asp Val Gln Leu Ala Gln Asp Asp Ile Asp Gly Ile  
 245 250 255

Gln Ala Ile Tyr Gly Arg Ser Gln Asn Pro Val Gln Pro Ile Gly Pro  
 260 265 270

Gln Thr Pro Lys Ala Cys Asp Ser Lys Leu Thr Phe Asp Ala Ile Thr  
 275 280 285

Thr Ile Arg Gly Glu Val Met Phe Phe Lys Asp Arg Phe Tyr Met Arg  
 290 295 300

Thr Asn Pro Phe Tyr Pro Glu Val Glu Leu Asn Phe Thr Ser Val Phe  
 305 310 315 320

Trp Pro Gln Leu Pro Asn Gly Leu Glu Ala Ala Tyr Glu Phe Ala Asp  
 325 330 335

Arg Asp Glu Val Arg Phe Phe Lys Gly Asn Lys Tyr Trp Ala Val Gln  
 340 345 350

Gly Gln Asn Val Leu His Gly Tyr Pro Lys Asp Ile Tyr Ser Ser Phe  
 355 360 365

Gly Phe Pro Arg Thr Val Lys His Ile Asp Ala Ala Leu Ser Glu Glu  
 370 375 380

Asn Thr Gly Lys Thr Tyr Phe Phe Val Ala Asn Lys Tyr Trp Arg Tyr  
385 390 395 400

Asp Glu Tyr Lys Arg Ser Met Asp Pro Gly Tyr Pro Lys Met Ile Ala  
405 410 415

His Asp Phe Pro Gly Ile Gly His Lys Val Asp Ala Val Phe Met Lys  
420 425 430

Asp Gly Phe Phe Tyr Phe Phe His Gly Thr Arg Gln Tyr Lys Phe Asp  
435 440 445

Pro Lys Thr Lys Arg Ile Leu Thr Leu Gln Lys Ala Asn Ser Trp Phe  
450 455 460

Asn Cys Arg Lys Asn  
465

<210> 13

<211> 468

<212> PRT

<213> Unknown

<220>

<223> X = UNKNOWN

<220>

<223> Description of Unknown Organism: Known Member of  
Matrix Metalloproteinase Family

<400> 13

Met Phe Ser Leu Lys Thr Leu Pro Phe Leu Leu Leu Leu His Val Gln  
1 5 10 15

Ile Ser Lys Ala Phe Pro Val Ser Ser Lys Glu Lys Asn Thr Lys Thr  
20 25 30

Val Gln Asp Tyr Leu Glu Lys Phe Tyr Gln Leu Pro Ser Asn Gln Tyr  
35 40 45

Gln Ser Thr Arg Lys Asn Gly Thr Asn Val Ile Val Glu Lys Leu Lys  
50 55 60

Glu Met Gln Arg Phe Phe Gly Leu Asn Val Thr Gly Lys Pro Asn Glu  
65 70 75 80

Glu Thr Leu Asp Met Met Lys Lys Pro Arg Cys Gly Val Pro Asp Ser	85	90	95
Gly Gly Phe Met Leu Thr Pro Gly Asn Pro Lys Trp Glu Arg Thr Asn	100	105	110
Leu Thr Tyr Arg Ile Arg Asn Tyr Thr Pro Gln Leu Ser Glu Ala Glu	115	120	125
Val Glu Arg Ala Ile Lys Asp Ala Phe Glu Leu Trp Ser Val Ala Ser	130	135	140
Pro Leu Ile Phe Thr Arg Ile Ser Gln Gly Glu Ala Asp Ile Asn Ile	145	150	155
Ala Phe Tyr Gln Arg Asp His Gly Asp Asn Ser Pro Phe Asp Gly Pro	165	170	175
Asn Gly Ile Leu Ala His Ala Phe Gln Pro Gly Gln Gly Ile Gly Gly	180	185	190
Asp Ala His Phe Asp Ala Glu Glu Thr Trp Thr Asn Thr Ser Ala Asn	195	200	205
Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe Gly His Ser Leu Gly	210	215	220
Leu Ala His Ser Ser Asp Pro Gly Ala Leu Met Tyr Pro Asn Tyr Ala	225	230	235
Phe Arg Glu Thr Ser Asn Tyr Ser Leu Pro Gln Asp Asp Ile Asp Gly	245	250	255
Ile Gln Ala Ile Tyr Gly Leu Ser Ser Asn Pro Ile Gln Pro Thr Gly	260	265	270
Pro Ser Thr Pro Lys Pro Cys Asp Pro Ser Leu Thr Phe Asp Ala Ile	275	280	285
Thr Thr Leu Arg Gly Glu Ile Leu Phe Phe Lys Asp Arg Tyr Phe Trp	290	295	300
Arg Arg His Pro Gln Leu Gln Arg Val Glu Met Asn Phe Ile Ser Leu	305	310	315
Phe Trp Pro Ser Leu Pro Thr Gly Ile Gln Ala Ala Tyr Glu Asp Phe	325	330	335

Asp Arg Asp Leu Ile Phe Leu Phe Lys Gly Asn Gln Tyr Trp Ala Leu  
340 345 350

Ser Gly Tyr Asp Ile Leu Gln Gly Tyr Pro Lys Asp Ile Ser Asn Tyr  
355 360 365

Gly Phe Pro Ser Ser Val Gln Ala Ile Asp Ala Ala Val Phe Tyr Arg  
370 375 380

Ser Lys Thr Tyr Phe Phe Val Asn Asp Gln Phe Trp Arg Tyr Asp Asn  
385 390 395 400

Gln Arg Gln Phe Met Glu Pro Gly Tyr Pro Lys Ser Ile Ser Gly Ala  
405 410 415

Phe Pro Gly Ile Glu Ser Lys Val Asp Ala Val Phe Gln Gln Glu His  
420 425 430

Phe Phe His Val Phe Ser Gly Pro Arg Tyr Tyr Ala Phe Asp Leu Ile  
435 440 445

Ala Gln Arg Val Thr Arg Val Ala Arg Gly Asn Lys Trp Leu Asn Cys  
450 455 460

Arg Tyr Gly Xaa  
465

<210> 14

<211> 476

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Known Member of  
Matrix Metalloproteinase Family

<400> 14

Met Met His Leu Ala Phe Leu Val Leu Leu Cys Leu Pro Val Cys Ser  
1 5 10 15

Ala Tyr Pro Leu Ser Gly Ala Ala Lys Glu Glu Asp Ser Asn Lys Asp  
20 25 30

Leu Ala Gln Gln Tyr Leu Glu Lys Tyr Tyr Asn Leu Glu Lys Asp Val  
35 40 45

Lys Gln Phe Arg Arg Lys Asp Ser Asn Leu Ile Val Lys Lys Ile Gln

50

55

60

Gly Met Gln Lys Phe Leu Gly Leu Glu Val Thr Gly Lys Leu Asp Thr  
65 70 75 80

Asp Thr Leu Glu Val Met Arg Lys Pro Arg Cys Gly Val Pro Asp Val  
85 90 95

Gly His Phe Ser Ser Phe Pro Gly Met Pro Lys Trp Arg Lys Thr His  
100 105 110

Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Arg Asp Ala  
115 120 125

Val Asp Ser Ala Ile Glu Lys Ala Leu Lys Val Trp Glu Glu Val Thr  
130 135 140

Pro Leu Thr Phe Ser Arg Leu Tyr Glu Gly Glu Ala Asp Ile Met Ile  
145 150 155 160

Ser Phe Ala Val Lys Glu His Gly Asp Phe Tyr Ser Phe Asp Gly Pro  
165 170 175

Gly His Ser Leu Ala His Ala Tyr Pro Pro Gly Pro Gly Leu Tyr Gly  
180 185 190

Asp Ile His Phe Asp Asp Asp Glu Lys Trp Thr Glu Asp Ala Ser Gly  
195 200 205

Thr Asn Leu Phe Leu Val Ala Ala His Glu Leu Gly His Ser Leu Gly  
210 215 220

Leu Phe His Ser Ala Asn Thr Glu Ala Leu Met Tyr Pro Leu Tyr Asn  
225 230 235 240

Ser Phe Thr Glu Leu Ala Gln Phe Arg Leu Ser Gln Asp Asp Val Asn  
245 250 255

Gly Ile Gln Ser Leu Tyr Gly Pro Pro Pro Ala Ser Thr Glu Glu Pro  
260 265 270

Leu Val Pro Thr Lys Ser Val Pro Ser Gly Ser Glu Met Pro Ala Lys  
275 280 285

Cys Asp Pro Ala Leu Ser Phe Asp Ala Ile Ser Thr Leu Arg Gly Glu  
290 295 300

Tyr Leu Phe Phe Lys Asp Arg Tyr Phe Trp Arg Arg Ser His Trp Asn

305                      310                      315                      320  
 Pro Glu Pro Glu Phe His Leu Ile Ser Ala Phe Trp Pro Ser Leu Pro  
                                  325                      330                      335  
 Ser Tyr Leu Asp Ala Ala Tyr Glu Val Asn Ser Arg Asp Thr Val Phe  
                                  340                      345                      350  
 Ile Phe Lys Gly Asn Glu Phe Trp Ala Ile Arg Gly Asn Glu Val Gln  
                                  355                      360                      365  
 Ala Gly Tyr Pro Arg Gly Ile His Thr Leu Gly Phe Pro Pro Thr Ile  
                                  370                      375                      380  
 Arg Lys Ile Asp Ala Ala Val Ser Asp Lys Glu Lys Lys Lys Thr Tyr  
 385                                   390                      395                      400  
 Phe Phe Ala Ala Asp Lys Tyr Trp Arg Phe Asp Glu Asn Ser Gln Ser  
                                  405                      410                      415  
 Met Glu Gln Gly Phe Pro Arg Leu Ile Ala Asp Asp Phe Pro Gly Val  
                                  420                      425                      430  
 Glu Pro Lys Val Asp Ala Val Leu Gln Ala Phe Gly Phe Phe Tyr Phe  
                                  435                      440                      445  
 Phe Ser Gly Ser Ser Gln Phe Glu Phe Asp Pro Asn Ala Arg Met Val  
                                  450                      455                      460  
 Thr His Ile Leu Lys Ser Asn Ser Trp Leu His Cys  
 465                                   470                      475

<210> 15  
 <211> 477  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: Known Member of  
                                  Matrix Metalloproteinase Family

<400> 15  
 Met Lys Ser Leu Pro Ile Leu Leu Leu Cys Val Ala Val Cys Ser  
   1                                 5                                 10                                 15

Ala Tyr Pro Leu Asp Gly Ala Ala Arg Gly Glu Asp Thr Ser Met Asn  
                                  20                                 25                                 30

Leu Val Gln Lys Tyr Leu Glu Asn Tyr Tyr Asp Leu Lys Lys Asp Val  
 35 40 45  
 Lys Gln Phe Val Arg Arg Lys Asp Ser Gly Pro Val Val Lys Lys Ile  
 50 55 60  
 Arg Glu Met Gln Lys Phe Leu Gly Leu Glu Val Thr Gly Lys Leu Asp  
 65 70 75 80  
 Ser Asp Thr Leu Glu Val Met Arg Lys Pro Arg Cys Gly Val Pro Asp  
 85 90 95  
 Val Gly His Phe Arg Thr Phe Pro Gly Ile Pro Lys Trp Arg Lys Thr  
 100 105 110  
 His Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Lys Asp  
 115 120 125  
 Ala Val Asp Ser Ala Val Glu Lys Ala Leu Lys Val Trp Glu Glu Val  
 130 135 140  
 Thr Pro Leu Thr Phe Ser Arg Leu Tyr Glu Gly Glu Ala Asp Ile Met  
 145 150 155 160  
 Ile Ser Phe Ala Val Arg Glu His Gly Asp Phe Tyr Pro Phe Asp Gly  
 165 170 175  
 Pro Gly Asn Val Leu Ala His Ala Tyr Ala Pro Gly Pro Gly Ile Asn  
 180 185 190  
 Gly Asp Ala His Phe Asp Asp Asp Glu Gln Trp Thr Lys Asp Thr Thr  
 195 200 205  
 Gly Thr Asn Leu Phe Leu Val Ala Ala His Glu Ile Gly His Ser Leu  
 210 215 220  
 Gly Leu Phe His Ser Ala Asn Thr Glu Ala Leu Met Tyr Pro Leu Tyr  
 225 230 235 240  
 His Ser Leu Thr Asp Leu Thr Arg Phe Arg Leu Ser Gln Asp Asp Ile  
 245 250 255  
 Asn Gly Ile Gln Ser Leu Tyr Gly Pro Pro Pro Asp Ser Pro Glu Thr  
 260 265 270  
 Pro Leu Val Pro Thr Glu Pro Val Pro Pro Glu Pro Gly Thr Pro Ala  
 275 280 285



Asn Cys Asp Pro Ala Leu Ser Phe Asp Ala Val Ser Thr Leu Arg Gly  
 290 295 300  
 Glu Ile Leu Ile Phe Lys Asp Arg His Phe Trp Arg Lys Ser Leu Arg  
 305 310 315 320  
 Lys Leu Glu Pro Glu Leu His Leu Ile Ser Ser Phe Trp Pro Ser Leu  
 325 330 335  
 Pro Ser Gly Val Asp Ala Ala Tyr Glu Val Thr Ser Lys Asp Leu Val  
 340 345 350  
 Phe Ile Phe Lys Gly Asn Gln Phe Trp Ala Ile Arg Gly Asn Glu Val  
 355 360 365  
 Arg Ala Gly Tyr Pro Arg Gly Ile His Thr Leu Gly Phe Pro Pro Thr  
 370 375 380  
 Val Arg Lys Ile Asp Ala Ala Ile Ser Asp Lys Glu Lys Asn Lys Thr  
 385 390 395 400  
 Tyr Phe Phe Val Glu Asp Lys Tyr Trp Arg Phe Asp Glu Lys Arg Asn  
 405 410 415  
 Ser Met Glu Pro Gly Phe Pro Lys Gln Ile Ala Glu Asp Phe Pro Gly  
 420 425 430  
 Ile Asp Ser Lys Ile Asp Ala Val Phe Glu Glu Phe Gly Phe Phe Tyr  
 435 440 445  
 Phe Phe Thr Gly Ser Ser Gln Leu Glu Phe Asp Pro Asn Ala Lys Lys  
 450 455 460  
 Val Thr His Thr Leu Lys Ser Asn Ser Trp Leu Asn Cys  
 465 470 475

<210> 16

<211> 708

<212> PRT

<213> Unknown

<220>

<223> X = UNKNOWN

<220>

<223> Description of Unknown Organism: Known Member of

# Matrix Metalloproteinase Family

<400> 16

Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys  
1 5 10 15

Cys Phe Ala Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro  
20 25 30

Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr  
35 40 45

Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser  
50 55 60

Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu  
65 70 75 80

Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr  
85 90 95

Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly  
100 105 110

Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr  
115 120 125

Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala  
130 135 140

Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr  
145 150 155 160

Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly  
165 170 175

Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe  
180 185 190

Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu  
195 200 205

Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn  
210 215 220

Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser  
225 230 235 240

Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys  
 245 250 255  
 Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro  
 260 265 270  
 Ser Glu Arg Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys  
 275 280 285  
 Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr  
 290 295 300  
 Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr  
 305 310 315 320  
 Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr  
 325 330 335  
 Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr  
 340 345 350  
 Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp  
 355 360 365  
 Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys  
 370 375 380  
 Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala  
 385 390 395 400  
 His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu  
 405 410 415  
 Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His  
 420 425 430  
 Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu  
 435 440 445  
 Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro  
 450 455 460  
 Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg  
 465 470 475 480  
 Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro  
 485 490 495

Pro Thr Ala Gly Pro Ser Thr Ala Thr Val Pro Leu Ser Pro Val  
500 505 510

Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly  
515 520 525

Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu  
530 535 540

Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp  
545 550 555 560

Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser  
565 570 575

Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly  
580 585 590

Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala  
595 600 605

Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met  
610 615 620

Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln  
625 630 635 640

Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly  
645 650 655

Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr  
660 665 670

Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu  
675 680 685

Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys  
690 695 700

Pro Glu Asp Xaa  
705

<210> 17

<211> 631

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Known Member of  
Matrix Metalloproteinase Family

<400> 17

Ala Pro Ser Pro Ile Ile Lys Phe Pro Gly Asp Val Ala Pro Lys Thr  
1 5 10 15

Asp Lys Glu Leu Ala Val Gln Tyr Leu Asn Thr Phe Tyr Gly Cys Pro  
20 25 30

Lys Glu Ser Cys Asn Leu Phe Val Leu Lys Asp Thr Leu Lys Lys Met  
35 40 45

Gln Lys Phe Phe Gly Leu Pro Gln Thr Gly Asp Leu Asp Gln Asn Thr  
50 55 60

Ile Glu Thr Met Arg Lys Pro Arg Cys Gly Asn Pro Asp Val Ala Asn  
65 70 75 80

Tyr Asn Phe Phe Pro Arg Lys Pro Lys Trp Asp Lys Asn Gln Ile Thr  
85 90 95

Tyr Arg Ile Ile Gly Tyr Thr Pro Asp Leu Asp Pro Glu Thr Val Asp  
100 105 110

Asp Ala Phe Ala Arg Ala Phe Gln Val Trp Ser Asp Val Thr Pro Leu  
115 120 125

Arg Phe Ser Arg Ile His Asp Gly Glu Ala Asp Ile Met Ile Asn Phe  
130 135 140

Gly Arg Trp Glu His Gly Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly  
145 150 155 160

Leu Leu Ala His Ala Phe Ala Pro Gly Thr Gly Val Gly Gly Asp Ser  
165 170 175

His Phe Asp Asp Asp Glu Leu Trp Thr Leu Gly Glu Gly Gln Val Val  
180 185 190

Arg Val Lys Tyr Gly Asn Ala Asp Gly Glu Tyr Cys Lys Phe Pro Phe  
195 200 205

Leu Phe Asn Gly Lys Glu Tyr Asn Ser Cys Thr Asp Thr Gly Arg Ser  
210 215 220

Asp Gly Phe Leu Trp Cys Ser Thr Thr Tyr Asn Phe Glu Lys Asp Gly

225		230		235		240
Lys Tyr Gly Phe Cys Pro His Glu Ala Leu Phe Thr Met Gly Gly Asn						
	245			250		255
Ala Glu Gly Gln Pro Cys Lys Phe Pro Phe Arg Phe Gln Gly Thr Ser						
	260		265			270
Tyr Asp Ser Cys Thr Thr Glu Gly Arg Thr Asp Gly Tyr Arg Trp Cys						
	275		280			285
Gly Thr Thr Glu Asp Tyr Asp Arg Asp Lys Lys Tyr Gly Phe Cys Pro						
	290		295			300
Glu Thr Ala Met Ser Thr Val Gly Gly Asn Ser Glu Gly Ala Pro Cys						
	305		310		315	320
Val Phe Pro Phe Thr Phe Leu Gly Asn Lys Tyr Glu Ser Cys Thr Ser						
		325		330		335
Ala Gly Arg Ser Asp Gly Lys Met Trp Cys Ala Thr Thr Ala Asn Tyr						
	340			345		350
Asp Asp Asp Arg Lys Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu						
	355		360			365
Phe Leu Val Ala Ala His Glu Phe Gly His Ala Met Gly Leu Glu His						
	370		375			380
Ser Gln Asp Pro Gly Ala Leu Met Ala Pro Ile Tyr Thr Tyr Thr Lys						
	385		390		395	400
Asn Phe Arg Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Glu Leu Tyr						
	405			410		415
Gly Ala Ser Pro Asp Ile Asp Leu Gly Thr Gly Pro Thr Pro Thr Leu						
	420			425		430
Gly Pro Val Thr Pro Glu Ile Cys Lys Gln Asp Ile Val Phe Asp Gly						
	435		440			445
Ile Ala Gln Ile Arg Gly Glu Ile Phe Phe Phe Lys Asp Arg Phe Ile						
	450		455			460
Trp Arg Thr Val Thr Pro Arg Asp Lys Pro Met Gly Pro Leu Leu Val						
	465		470		475	480
Ala Thr Phe Trp Pro Glu Leu Pro Glu Lys Ile Asp Ala Val Tyr Glu						

485

490

495

Ala Pro Gln Glu Glu Lys Ala Val Phe Phe Ala Gly Asn Glu Tyr Trp  
 500 505 510

Ile Tyr Ser Ala Ser Thr Leu Glu Arg Gly Tyr Pro Lys Pro Leu Thr  
 515 520 525

Ser Leu Gly Leu Pro Pro Asp Val Gln Arg Val Asp Ala Ala Phe Asn  
 530 535 540

Trp Ser Lys Asn Lys Lys Thr Tyr Ile Phe Ala Gly Asp Lys Phe Trp  
 545 550 555 560

Arg Tyr Asn Glu Val Lys Lys Lys Met Asp Pro Gly Phe Pro Lys Leu  
 565 570 575

Ile Ala Asp Ala Trp Asn Ala Ile Pro Asp Asn Leu Asp Ala Val Val  
 580 585 590

Asp Leu Gln Gly Gly Gly His Ser Tyr Phe Phe Lys Gly Ala Tyr Tyr  
 595 600 605

Leu Lys Leu Glu Asn Gln Ser Leu Lys Ser Val Lys Phe Gly Ser Ile  
 610 615 620

Lys Ser Asp Trp Leu Gly Cys  
 625 630

&lt;210&gt; 18

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

<223> Description of Unknown Organism: Known Member of  
 Matrix Metalloproteinase Family

&lt;400&gt; 18

Met Arg Leu Thr Val Leu Cys Ala Val Cys Leu Leu Pro Gly Ser Leu  
 1 5 10 15

Ala Leu Pro Leu Pro Gln Glu Ala Gly Gly Met Ser Glu Leu Gln Trp  
 20 25 30

Glu Gln Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu  
 35 40 45

Thr Lys Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys  
50 55 60

Phe Phe Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Arg Val Ile Glu  
65 70 75 80

Ile Met Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser  
85 90 95

Leu Phe Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg  
100 105 110

Ile Val Ser Tyr Thr Arg Asp Leu Pro His Ile Thr Val Asp Arg Leu  
115 120 125

Val Ser Lys Ala Leu Asn Met Trp Gly Lys Glu Ile Pro Leu His Phe  
130 135 140

Arg Lys Val Val Trp Gly Thr Ala Asp Ile Met Ile Gly Phe Ala Arg  
145 150 155 160

Gly Ala His Gly Asp Ser Tyr Pro Phe Asp Gly Pro Gly Asn Thr Leu  
165 170 175

Ala His Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe  
180 185 190

Asp Glu Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe  
195 200 205

Leu Tyr Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His  
210 215 220

Ser Ser Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp  
225 230 235 240

Pro Gln Asn Phe Lys Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Lys  
245 250 255

Leu Tyr Gly Lys Arg Ser Asn Ser Arg Lys Lys  
260 265

<210> 19

<211> 231

<212> PRT

<213> Unknown



<220>

<223> Description of Unknown Organism: Known Member of  
Matrix Metalloproteinase Family

<400> 19

Met Pro Leu Leu Leu Leu Leu Glu Tyr Leu Glu Lys Leu Met Gln Lys  
1 5 10 15

Phe Gly Leu Val Thr Gly Lys Leu Asp Thr Leu Met Arg Lys Pro Arg  
20 25 30

Cys Gly Val Pro Asp Val Gly Phe Phe Pro Gly Pro Lys Trp Thr Leu  
35 40 45

Thr Tyr Arg Ile Asn Tyr Thr Pro Asp Leu Pro Val Asp Ala Lys Ala  
50 55 60

Phe Val Trp Ser Val Thr Pro Leu Thr Phe Arg Val Glu Gly Ala Asp  
65 70 75 80

Ile Met Ile Phe Ala His Gly Asp Tyr Pro Phe Asp Gly Pro Gly Gly  
85 90 95

Leu Ala His Ala Phe Pro Gly Pro Gly Ile Gly Gly Asp Ala His Phe  
100 105 110

Asp Asp Glu Trp Thr Asn Leu Phe Leu Val Ala Ala His Glu Gly His  
115 120 125

Ser Leu Gly Leu His Ser Asp Pro Ala Leu Met Tyr Pro Thr Phe Phe  
130 135 140

Leu Ser Gln Asp Asp Ile Gly Ile Gln Leu Tyr Gly Pro Pro Thr Cys  
145 150 155 160

Asp Phe Asp Ala Ile Thr Arg Gly Glu Phe Phe Lys Asp Arg Trp Arg  
165 170 175

Leu Ser Phe Trp Pro Leu Pro Asp Ala Ala Tyr Glu Phe Phe Gly Asn  
180 185 190

Tyr Trp Gly Gly Tyr Pro Ile Leu Gly Pro Val Asp Ala Ala Lys Thr  
195 200 205

Tyr Phe Phe Lys Trp Arg Asp Met Pro Gly Pro Ile Phe Pro Gly Asp  
210 215 220

Ala Val Phe Phe Trp Leu Cys  
225 230

Ala Val Phe Phe Trp Leu Cys  
225 230